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OM protein - protein search, using sw model

Run on: June 23, 2003, 15:04:31 ; Search time 23 Seconds  
(without alignments)  
331.811 Million cell updates/sec

Title: AAK91826

Perfect score: 965  
Sequence: 1 MKRGRSLRGDPAPPTCV.....ATELGSTELVTKTAGPEQO 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	965	100.0	184	T13C_HUMAN	Q96TJ3 homo sapien
2	410.5	42.5	175	T13C_MOUSE	Q96TJ3 mus musculu
3	124	12.8	439	XP2_XENLA	P17437 xenopus lae
4	120.5	12.5	1083	T2D3_HUMAN	O00268 homo sapien
5	116.5	12.1	676	ICP0_HSVBJ	P29128 bovine herp
6	109	11.3	325	DBP_HUMAN	O10586 homo sapien
7	107	11.1	2142	BAT2_HUMAN	P48534 homo sapien
8	106.5	11.0	356	HXB2_HUMAN	P14652 homo sapien
9	103	10.7	505	WASH_BOVIN	Q95107 bos taurus
10	102.5	10.6	676	ICP0_HSVBK	P29836 bovine herp
11	102.5	10.6	725	AREA_PENCH	O01582 penicillium
12	102	10.6	317	YQ35_CAEEL	O09456 caenorhabd
13	102	10.6	325	DBP_MOUSE	O60925 mus musculu
14	102	10.6	325	DBP_RAT	P16443 rattus norv
15	99.5	10.3	503	ICP7_HUMAN	Q92985 homo sapien
16	99	10.3	1487	ICP4_HSVB	P28925 equine herp
17	98	10.2	684	CA39_HUMAN	O14050 homo sapien
18	98	10.2	1487	ICP4_HSVK	P17473 equine herp
19	97.5	10.1	384	VASP_CNFA	P50551 canis fami
20	97.5	10.1	915	AL80_RAT	O05490 pseudomona
21	97	10.1	353	LICH_PSEGL	O97423 mus musculu
22	97	10.1	1229	NI21_HUMAN	O08608 mus musculu
23	96.5	10.0	1255	DIA1_MOUSE	O97566 homo sapien
24	96	9.9	2161	SHK1_HUMAN	O97566 homo sapien
25	96	9.9	3164	TEGU_HSV11	Q91820 herpes simp
26	95.5	9.9	129	FN14_HUMAN	Q91820 herpes simp
27	95.5	9.9	416	CC07_CAEEL	P18832 caenorhabd
28	95	9.8	312	CBX6_HUMAN	O95503 caenorhabd
29	95	9.8	625	DUS8_HUMAN	O13302 homo sapien
30	95	9.8	722	Z219_HUMAN	O92474 homo sapien
31	95	9.8	776	SM4F_RAT	Q92143 rattus norv
32	95	9.8	1248	DIA1_HUMAN	O60610 homo sapien
33	95	9.8	1509	GSRI_HUMAN	Q9azm4 homo sapien

34	94.5	9.8	374	1	PSPD_MOUSE	P50404 mus musculu
35	94.5	9.8	449	1	APG_BRANA	P40603 brassica na
36	94.5	9.8	1838	1	CA15_HUMAN	P20908 homo sapien
37	94	9.7	263	1	ICP3_HSV1F	P08353 herpes simp
38	94	9.7	654	1	SPH2_HUMAN	Q91ra0 homo sapien
39	94	9.7	777	1	SM4F_MOUSE	Q92123 mus musculu
40	94	9.7	806	1	MK07_MOUSE	Q92949 homo sapien
41	93.5	9.7	421	1	FXJ1_HUMAN	O13164 homo sapien
42	93.5	9.7	815	1	MK07_HUMAN	O15534 homo sapien
43	93.5	9.7	1290	1	PER1_HUMAN	O02223 homo sapien
44	93	9.6	184	1	TR17_HUMAN	O88472 mus musculu
45	93	9.6	185	1	TR17_MOUSE	

## ALIGNMENTS

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RESULT 1
ID      T13C_HUMAN          STANDARD;          PRT;          184 AA.
AC      Q96TJ3;
DT      15-JUN-2002 (rel. 41, last, sequence update)
DT      15-JUN-2002 (rel. 41, last, annotation update)
DE      Tumor necrosis factor receptor superfamily member 13C (B cell-
DE      activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
DE      3).
GN      TNFRSF13C OR BAFFR OR BR3.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_Taxid:9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC      TISSUE=B-cell lymphoma;
RX      MEDLINE=21442025; PubMed=11509692;
RA      Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA      Cachero T.G., Hession C., Schneider P., Sizung I.D., Mullen C.,
RA      Strauch K., Zafari M., Benjamin C.D., Teschopp J., Browning J.L.,
RA      Ambrose C., a newly identified TNF receptor that specifically interacts
RA      with BAFF-R.
RT      Science 293:2108-2111 (2001).
RL      [2]
RN      [2]
RP      FUNCTION.
RX      MEDLINE=21475520; PubMed=11591325;
RA      Yan W., Brady J.R., Chan B., Lee W.P., Hsu B., Hartless S.M.,
RA      Canero M.P., Grewal I.S., Dixit V.M.;
RT      Identification of a novel receptor for B lymphocyte stimulator that
RT      is mutated in a mouse strain with severe B cell deficiency.
RL      Curr. Biol. 11:1547-1552 (2001).
CC      - FUNCTION: B-cell receptor specific for TNFRSF1B/TNLF/BAFF/Blys.
CC      Promotes the survival of mature B-cells and the B-cell response.
CC      - SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC      - ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
CC      produced by alternative splicing.
CC      - TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
CC      in resting CD4+ T-cells. Detected at lower levels in activated B-cells,
CC      in resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
CC      - SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
DR      EMBL, AF373846; AAK91826.1;
DR      GenBank, HGNC:17755; TNFRSF13C.
DR      MIM, 606269;
DR      PROSITE, PS00652; TNFR_NGFR_1; FALSE_NEG.

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DR PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.  
 KM Receptor; Immune response; Signal-anchor; Transmembrane;  
 KW Alternative splicing 78  
 FT DOMAIN 1  
 FT TRANSMEM 79 99  
 FT SIGNAL-ANCHOR (POTENTIAL)  
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)  
 FT DOMAIN 100 184  
 FT REPEAT 18 35  
 FT DISULFID 19 32  
 FT DISULFID 24 35  
 FT VARSPPLIC 143 143  
 FT P -> FA (IN ISOFORM 2).  
 SQ SEQUENCE 184 AA; 18863 MW; F2BFB98099A27138 CRC64;  
 Query Match 100.0%; Score 965; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1e-56;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRGPRSLGRDAPAPTPCVPAECFDLVNHCYACGLLTPRDKPKAGASSPAPRTALQPO 60  
 DB 1 MRGPRSLGRDAPAPTPCVPAECFDLVNHCYACGLLTPRDKPKAGASSPAPRTALQPO 60  
 DB 61 ESYGAGAGEAALPLPGILFGAPALLGLALVLAIVLGLVSWRRORRLKAGASAEAPDGD 120  
 DB 61 ESYGAGAGEAALPLPGILFGAPALLGLALVLAIVLGLVSWRRORRLKAGASAEAPDGD 120  
 QY 121 KDAPELDKVIILSPGISDAPAMPPEGEPGTPPGHSPVPATELGSTELVTKTAG 180  
 DB 121 KDAPELDKVIILSPGISDAPAMPPEGEPGTPPGHSPVPATELGSTELVTKTAG 180  
 QY 181 PEGQ 184  
 DB 181 PEGQ 184  
 DB 181 PEGQ 184  
 RESULT 2  
 ID T13C.MOUSE STANDARD; PRT; 175 AA.  
 AC Q9DBD0;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3) (B-cell maturation defect).  
 GN TNFRSF13C OR BAFFR OR BCMD OR BR3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 (1)  
 RC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN=BA1B/C; TISSUE=B-cell lymphoma;  
 RX MEDLINE=21442025; PubMed=11509692;  
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizling I.D., Millen C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L., Ambrose C.;  
 RA "BAFF-R, a newly identified TNF receptor that specifically interacts with BAFF.";  
 RT Science 293:2108-2111(2001).  
 RN (2)  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.  
 RC STRAIN=A/J;  
 RX MEDLINE=21475520; PubMed=11591325;  
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;  
 RA "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";  
 RT Curr. Biol. 11:1547-1552(2001).  
 RN (3)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=C57BL/60; TISSUE=Small intestine;  
 RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojohori T., Bono H., Kanakawa T., Saito R., Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bersh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.T., Bult C., Fletcher C., Fujita M., Gariboldi M., Gasteig J., Hall D., Hofmann M., Hume D.A., Kamita M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S., Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RT Nature 409:685-690(2001).  
 RN (4)  
 RP FUNCTION.  
 RX MEDLINE=21614654; PubMed=11747827;  
 RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K., Hilbert D.M., Hayes C.E., Cancro M.P.;  
 RA "Competition for Blys-mediated signaling through Bcmd/BR3 regulates peripheral B lymphocyte numbers.";  
 RT Curr. Biol. 11:1986-1989(2001).  
 CC -1- FUNCTION: B-cell receptor specific for TNFRSF1B/TNFI/BAFF/Blys.  
 CC Promotes the survival of mature B-cells and the B-cell response.  
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (probable).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;  
 CC detected at lower levels in lung and thymus.  
 CC -1- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell deficiency. B-cell deficient strain A/WySn has a 4.7 kb insertion in the BAFFR gene leading to an altered C-terminal. The mutant RNA is not detectable. B-cell lymphopoeisis is normal, but the life span of peripheral B-cells is much reduced.  
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.  
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 CC -----  
 DR EMBL; AF373847; AAK91827.1; -;  
 DR EMBL; AK008142; BAB25490.1; -;  
 DR MGD; MGI:1919299; Tnfrsf13c.  
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein; Alternative splicing.  
 FT DOMAIN 1 71  
 FT TRANSMEM 72 92  
 FT SIGNAL-ANCHOR (POTENTIAL)  
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)  
 FT DOMAIN 93 175  
 FT REPEAT 21 38  
 FT DISULFID 22 35  
 FT DISULFID 27 38  
 FT CARBOHYD 23 23  
 FT VARSPPLIC 133 143  
 FT MISSING (IN ISOFORM 2).  
 SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;  
 Query Match 42.5%; Score 410.5; DB 1; Length 175;  
 Best Local Similarity 56.1%; Pred. No. 1.9e-21;  
 Matches 101; Conservative 9; Mismatches 55; Indels 15; Gaps 6;  
 QY 6 RSLRGDAPAPTPCVPAECFDLVNHCYACGLLTPRDKPKAGASSPAPRTALQPOESVVA 65  
 DB 9 RSLRGDAPAPTPCVPAECFDLVNHCYACGLLTPRDKPKAGASSPAPRTALQPOE----- 62

QY 66 GAGEALPLPGLLFGAPALLGLALVIALV-LVGLVSWRRRRLRGASSAEPDGDKDA-123  
 DB 63 --GSLRPFVALVGAAPALLGLIALTLVGLVSWRRRQ-QLRTAS----PDTSSEVQ 115  
 QY 124 PEPLDKVILLSPGISDATPAMPPEDEDPCTTPPGHVSVPVATLSTELVTTKNGPQ 183  
 DB 116 QESLENVFVPSSETPHASAPTWPELKEADSLPRHSVVPATELGSTELVTTKNGPQ 175

RESULT 3  
 XP2\_XENLA STANDARD; PRT; 439 AA.  
 ID XP2\_XENLA  
 AC P17437; Q08944; 01-AUG-1990 (Rel. 15, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Skin secretory protein XP2 precursor (APB protein).  
 Xenopus laevis (African clawed frog).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 Xenopodinae; Xenopus.  
 NCBI\_Taxid=8355;  
 OC NCBTAXID=8355;  
 RP SEQUENCE OF 1-25 AND 344-439 FROM N.A. (ISOFORM 2).  
 RX MEDLINE=92332564; PubMed=1629230;  
 RA Hauser F., Roeben C., Hoffmann W.;  
 RT "XP2, a new member of the P-domain peptide family of potential growth  
 RL factors, is synthesized in Xenopus laevis skin."  
 RL J. Biol. Chem. 267:14451-14455(1992).  
 RN [2]  
 RC SEQUENCE OF 3-439 FROM N.A. (ISOFORM 1).  
 RC TISSUE=Skin;  
 RX MEDLINE=90127399; PubMed=2298293;  
 RA Gmachl M., Berger H., Thalhammer U., Kreil G.;  
 RT "Dermal glands of Xenopus laevis contain a polypeptide with a highly  
 RL repetitive amino acid sequence."  
 RL FEBS Lett. 260:145-148(1990).  
 CC -1- FUNCTION: MAY ACT AS A GROWTH FACTOR IN THE GERMINAL LAYER OF THE  
 CC EPIDERMIS. MAY ALSO BE INVOLVED IN GROWTH OF REGENERATING GLANDS  
 CC AND IN PROTECTION OF THE SKIN FROM THE EXTERNAL ENVIRONMENT.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ABEG (shown here) and 2/XP2;  
 CC are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: SKIN.  
 CC -1- SIMILARITY: CONTAINS 2 P-TYPE (TREFOL) DOMAINS  
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 392  
 CC ONWARD AND IS SHORTER (418 AA) DUE TO A FRAMESHIFT.  
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 CC -----  
 CC EMBL M90095; AA50001.1; -  
 CC EMBL X51394; CA35759.1; ALT\_FRAME.  
 CC FIR; S07498; SKLKG.  
 CC DR PIR; A37331; A37331.  
 CC DR HSSP; P04155; 1PS2.  
 CC DR InterPro; IPR000519; P\_trefol.  
 CC Pfam; PF00088; trefol.2.  
 CC DR PRINTS; PR00680; FTREFOL.  
 CC DR SMART; SM00018; P\_2.  
 CC DR PROSITE; PS00025; P\_TREFOL; 2.  
 CC Signal; Growth factor; Alternative splicing; Amphibian skin; Repeat.  
 CC SIGNAL 1 22 POTENTIAL.  
 CC MOD RES 23 439 SKIN SECRETORY PROTEIN XP2.  
 CC MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).  
 CC MOD RES 26 343 33 X REPEATS OF G-[GE]-[AP] (2,4)-A-B.  
 CC DOMAIN 350 391 P-TYPE 1.

FT DOMAIN 397 438 P-TYPE 2.  
 FT DISULFID 351 377 BY SIMILARITY.  
 FT DISULFID 361 376 BY SIMILARITY.  
 FT DISULFID 371 388 BY SIMILARITY.  
 FT DISULFID 398 424 BY SIMILARITY.  
 FT DISULFID 408 423 BY SIMILARITY.  
 FT DISULFID 418 435 BY SIMILARITY.  
 FT VARSPLIC 26 343 MISSING (IN ISOFORM 2).  
 FT CONFLICT 3 3 H -> S (IN REF. 2).  
 FT CONFLICT 18 18 C -> W (IN REF. 2).  
 SQ SEQUENCE 439 AA; 41173 MW; 38C4A4B57CBAE778 CRC64;

Query Match 12.8%; Score 124; DB 1; Length 439;  
 Best Local Similarity 27.5%; Pred. No. 0.08;  
 Matches 46; Conservative 10; Mismatches 57; Indels 54; Gaps 7;

QY 12 DAPAPTPC-----VPACFDLVKHCVCGLTTPPKPGAGSPAPRTLOPQESVG 64  
 DB 155 EAPAPAPAEVEAPAPAPAEAG-----EAPAPAPAEAGAPAPAPAEAGAPAPA 200  
 QY 65 AGAGEALPLPGLLFGAPALLGLALVIALV-LVGLVSWRRRRLRGASSAEPDGDKDA 123  
 DB 201 PAEGEPAPAP-----APA-----EGEAPAPAPAEAGAPA 230

QY 124 PEPLD-KVILLSPGISDATPAMPPEDEDPCTTPPGHVSVPVATLSTELVTTKNGPQ 169  
 DB 231 PAPAGEAPAPAPAPAEAGAPAPA-PAEGEPAPAPAPAEAGAPAPAPAEAG 276

RESULT 4  
 ID T2D3\_HUMAN STANDARD; PRT; 1083 AA.  
 AC 000268; Q99721; Q9BX42; Q9BR40;  
 DT 15-JUN-1998 (Rel. 35, Created)  
 DT 15-JUN-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Transcription initiation factor TFIID 135 kDa subunit (TAFII-135)  
 GN TAFII135 (TAFII-130) (TAFII130).  
 OS TAFA OR TAFA4 OR TAF2C1 OR TAF2C OR TAFII135 OR TAFII130.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBTAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97336072; PubMed=9192867;  
 RA Wengus G., May M., Carre L., Chandon P., Davidson I.;  
 RT "Human TAF(II)135 potentiates transcriptional activation by the AF-2s  
 RT of the retinoic acid, vitamin D3, and thyroid hormone receptors in  
 RL mammalian cells."  
 RL Genes Dev. 11:1381-1395(1997).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,  
 RA Bailey O.P., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.B., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Dearden R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley U.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Levasaiho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Philimore B.J.C.T., Prichalngam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhan R., Sims S.,

```

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whitcaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RT Nature 414:865-871(2001).
RL
RN
RP
RP SEQUENCE OF 105-1083 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=9708442; PubMed=8942982;
RA Tanese N., Saluja D., Vassallo M.F., Chen J.-L., Admon A.;
RT "Molecular cloning and analysis of two subunits of the human TFIIID
complex: hTAFII10 and hTAFII100.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13611-13616(1996).
CC
CC -1- FUNCTION: MAKES PART OF TFIIID IS A MULTIMERIC PROTEIN COMPLEX THAT
CC PLAYS A CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS
CC ACTIVATORS AND REPRESSORS. POTENTIATES TRANSCRIPTIONAL ACTIVATION
CC BY THE AP-2S OF THE RETINOIC ACID, VITAMIN D3 AND THYROID HORMONE.
CC -1- SUBUNIT: TFIIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
CC NUMBER OF TBP-ASSOCIATED FACTORS (TAFs).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE TAF2C FAMILY.
CC -----
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CC -----
DR EMBL, Y11354; CA72189.1; -
DR EMBL, AL137077; CAC36006.1; -
DR EMBL, AL109911; CAC23312.2; -
DR EMBL, U75308; AAC50901.1; -
DR TRANSFAC; T02328; -
DR Genew; HGNC:11537; TAF4.
DR MIM; 601796; -
DR InterPro; IPR003894; TAF_hom.
DR SMART; SMO0549; TAF1.1.
KW Transcription regulation; Nuclear protein.
FT DOMAIN 39 42 POLY-HIS.
FT FT 52 57 POLY-ALA.
FT FT 98 101 POLY-GLY.
FT FT 142 148 POLY-ALA.
FT FT 268 275 POLY-PRO.
FT FT 331 337 POLY-ALA.
FT FT 680 683 POLY-PRO.
FT FT 808 813 POLY-ALA.
FT FT 828 831 POLY-ASP.
FT FT 105 117 PPSPPRRPLVPA -> GRGLLQORGRRES
FT FT (IN REF. 3).
FT FT CONFLICT 136 136 A -> S (IN REF. 2).
FT FT CONFLICT 185 185 G -> GPG (IN REF. 2).
FT FT CONFLICT 233 264 MISSING (IN REF. 3).
FT FT CONFLICT 293 293 P -> L (IN REF. 3).
SO SEQUENCE 1083 AA; 109943 MW; A6453827572A0752 CRC64;

Query Match 12.5%; Score 120.5; DB 1; Length 1083;
Beet Local Similarity 27.4%; Pred. No. 0.31;
Matches 63; Conservative 11; Mismatches 99; Indels 63; Gaps 9;

OY 2 RRGPRSLGRDAPAPTPCVPA-----ECFDLLVHHCYACGLLRTTPRKPAGAS 49
DB 104 RPPGPPSPRRPLVPA-GPAAPPAKLRPPPEGAGACAPVPAANAAG---PPAPAPGA 158
OY 50 SPAPRTALQPPESVGAGGAAALPLPG-----LIFGAPALL----- 85
DB 159 KPAPGPAALAAAGAPGPGPGPGPGPGAPGAPGAQTLNGSAALLNHHAAAPVSLVNN 218
OY 86 GLALVLAIVLVGLVSWRRRRRLRGASSAEPDGDKDAPEFLDRIYILSPGISDAPAW 145

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Db      219  GPALLLPLPKRAAGTGIQTPEPFVGAAPAPAP-----AASPAPAPAPAP-----AAAPP 270
Oy      146  PPEPDEGCTTPRGH-----SVPPAT-----ELGSTELVTTKTAGP 181
Db      271  PEPAPATLAPPGHAGPPTAAPAVPPPPAAANQNGSAGAAPAPAPAAAGP 320

RESULT 5
ICP0_HSVBJ
ID      ICP0_HSVBJ  STANDARD;  PRT;  676 AA.
AC      P29128;
DT      01-DEC-1992 (Rel. 24, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Trans-acting transcriptional protein ICP0 (p135 protein) (IER
DE      2.9/ER2.6).
GN      BICP0.
OS      Bovine herpesvirus type 1 (strain Jura).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Alphaherpesvirinae; Varicellovirinae.
NCBI_TaxID=31518;
[1]
SEQUENCE FROM N.A.
RP      MEDLINE=92219360; PubMed=1313901;
RX      Wirth U.V., Fraefel C., Vogt B., Vilek C., Paces V., Schwyzer M.;
RT      "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1
RT      are 3' coterminal and encode a putative zinc finger transactivator
RT      protein."
RL      J. Virol. 66:2763-2772(1992).
CC      -1- PPM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL
CC      ACTIVATION DOMAIN, POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY
CC      CASEIN KINASE II.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      -1- SIMILARITY: TO OTHER HERPESVIRUSES ICP0 PROTEIN.
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-----
DR      EMBL; M84465; AAA46062.1; -.
DR      EMBL; AJ004801; CA006138.1; -.
DR      PIR; B38209; EDBE23.
DR      HSSP; P28990; ICHC.
DR      InterPro; IPR001841; Znf_ring.
DR      Pfam; PF00097; zf-C3HC4; 1.
DR      SMART; SMO0184; RING; 1.
DR      PROSITE; PS00518; ZF_RING_1; 1.
DR      PROSITE; PS50089; ZF_RING_2; 1.
KW      Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
KW      DNA-binding; Early protein; Repressor; Phosphorylation.
KW      ZN_FING 13
KW      FT 52
KW      DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).
SO      SEQUENCE 676 AA; 67879 MW; 11B05BA85C4EB71 CRC64;

Query Match 12.1%; Score 116.5; DB 1; Length 676;
Best Local Similarity 30.4%; Pred. 0.38;
Matches 62; Conservative 13; Mismatches 78; Indels 51; Gaps 11;

Oy      7  SLRRDAPATPCVPACPFLLVRHCACG-----LRTTPPKP 45
Db      353  STRGRQTPAOPAPRS-----LARR--PCGRAAVASPSSRSRGRRDRPLPAAPAPAP 405
Oy      46  AG---ASSPAPRTALQGESVAGAGAGAAALPLPGLLFGAALALGLALVLALVVG---LV 99
Db      406  AAQARACSPSPR-----EEGRGAGLGVAAAGETAGWGAGSGEGRGERARLLLGAGPPRPVQ 460
Oy      100  SWRRRQRRLRGASSAAPDGDGDAPEDLKVIIILSPGISDATA-PAMPPEGEDPGTTPP 157
Db      461  ARRRRRRELTDRAPTPAPAP---APAPPISTVIDLT---ANAPAPADPAPAAAPGASAA 514

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QY 158 GHSVPATGTELGSTELVTKTAGP 181  
 DB 515 GAQIGTPA-----AAAATTAATAAP 534

RESULT 6  
 DBP\_HUMAN STANDARD; PRT; 325 AA.  
 AC 010586;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE D-site-binding protein (Albumin D box-binding protein) (TAXREB302).  
 GN DBP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=95137580; PubMed=7835883;  
 RA Khatib Z.A., Inaba T., Valentine M., Look A.T.;  
 RT "Chromosomal localization and cDNA cloning of the human DBP and TEF  
 genes.";  
 RL Genomics 23:344-351(1994).  
 [2]  
 SEQUENCE FROM N.A.  
 MEDLINE=96377425; PubMed=8786133;  
 RA Shults G., Glasco T., Kang X., Korneluk R., Mueller C.R.;  
 RT "Genomic structure of the human D-site binding protein (DBP) gene.";  
 RL Genomics 34:334-339(1996).  
 [3]  
 SEQUENCE FROM N.A.  
 TISSUE=Brain;  
 MEDLINE=97264341; PubMed=9110174;  
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,  
 RA Riccietre J.Y., Wentland M.A., Lennon G., Gibbs R.A.;  
 RT "Large-scale concatenation cDNA sequencing.";  
 RL Genome Res. 7:353-358(1997).  
 [4]  
 SEQUENCE OF 132-325 FROM N.A.  
 MEDLINE=93246252; PubMed=8482542;  
 RA Nyunoya H., Morita T., Sato T., Honma S., Tsujimoto A.,  
 RA Shimotohno K.;  
 RT "Cloning of a cDNA encoding a DNA-binding protein TAXREB302 that is  
 specific for the tax-responsive enhancer of HTLV-I.";  
 RL Gene 126:251-255(1993).  
 [5]  
 REVISIONS.  
 RA Nyunoya H.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 [6]  
 REVIEW.  
 MEDLINE=9439627; PubMed=10508692;  
 RA Brown S.A., Schibler U.;  
 RT "The ins and outs of circadian timekeeping.";  
 RL Curr. Opin. Genet. Dev. 9:588-594(1999).  
 -1- FUNCTION: THIS TRANSCRIPTIONAL ACTIVATOR RECOGNIZES AND BINDS TO  
 THE SEQUENCE 5'-RTTAGTAA-3' FOUND IN THE PROMOTER OF GENES SUCH  
 AS ALBUMIN, CYP2A4 AND CYP2A5. IT IS NOT ESSENTIAL FOR CIRCADIAN  
 RHYTHM GENERATION, BUT MODULATES IMPORTANT CLOCK OUTPUT GENES. MAY  
 BE A DIRECT TARGET FOR REGULATION BY THE CIRCADIAN PACEMAKER  
 COMPONENT CLOCK. MAY AFFECT CIRCADIAN PERIOD AND SLEEP REGULATION.  
 -1- SUBUNIT: BINDS DNA AS A HOMODIMER OR A HETERODIMER. CAN FORM A  
 HETERODIMER WITH TEF.  
 -1- SUBCELLULAR LOCATION: Nuclear.  
 -1- TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED. EXPRESSED IN THE  
 SUPRACHIASMATIC NUCLEI (SCN) AND IN MOST PERIPHERAL TISSUES, WITH  
 A STRONG CIRCADIAN RHYTHMICITY.  
 -1- SIMILARITY: BELONGS TO THE BZIP FAMILY. PAR SUBFAMILY.  
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 CC -----  
 CC EMBL: U06936; AAA81374.1; -  
 CC DR EMBL, U48213; AAB18668.1; -  
 CC DR EMBL, U48212; AAB18668.1; JOINED.  
 CC DR EMBL, U79283; AAB50219.1; -  
 CC DR EMBL, D28468; BAA05833.1; -  
 CC DR TRANSFAC; T04875; -  
 CC DR Genew; HGNC:2697; DBP.  
 CC MIM: 124097; -  
 CC DR InterPro; IPR004827; TF\_BZIP.  
 CC DR SMART; SM00338; BRLZ; 1.  
 CC KW DNA-binding; Transcription regulation; Activator; Nuclear protein;  
 CC Biological rhythms.  
 CC FT DOMAIN 129 135 POLY-PRO.  
 CC FT DOMAIN 188 239 PRO-RICH (PROLINE/ACIDIC REGION (PAR)).  
 CC FT DNA BIND 258 277 BASIC MOTIF.  
 CC FT DOMAIN 250 304 LEUCINE-ZIPPER.  
 CC FT CONFLICT 179 179 S -> T (IN REF. 1).  
 CC FT CONFLICT 245 245 R -> K (IN REF. 4).  
 CC SQ SEQUENCE 325 AA; 34349 MW; A6933CE21399ECF3 CRC64;  
 Query Match 11.3%; Score 109; DB 1; Length 325;  
 Best Local Similarity 27.1%; Pred. No. 0.62; Indels 62; Gaps 9;  
 Matches 56; Conservative 12; Mismatches 77;  
 QY 4 GPRSLRGDAPAPTCVPA-----ECFDL---LVKHCVCAGLARTPPKPG 47  
 DB 83 GGGSPRGPRGPVPAAGLAAPLMERTLPQGVYVDLAFLEH---GL--PPSPPPG 136  
 QY 48 ASSPAPRTALPOQESVAGAGEALP--LPGLLFAPALLGLVLAIVGLVSWRRQ 105  
 DB 137 GSPSPAPRTPAPSPGSCSASPRSPG---HAPRAALGT----- 177  
 QY 106 RRLRGASSAEAPDGKADPELDKYLISPGISDAITAAWPPRGDPTTPGHSVPVA 165  
 DB 178 ----ASGHRAGLTNRDTPSPVD-----PDTVEVLMTFEPPDPAULASLPGHETPDR 226  
 QY 166 TELGSTELY-----TTKTAGPEQ 184  
 DB 227 RHRFSEELKPOPIMKAKKIOVPEEQ 253

RESULT 7  
 BAT2\_HUMAN STANDARD; PRT; 2142 AA.  
 AC P48634;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Large proline-rich protein Bat2 (HLA-B-associated transcript 2).  
 GN BAT2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=T-cell;  
 MEDLINE=90192810; PubMed=2156268;  
 RA Banerji J., Sands J., Strominger J.L., Spies T.;  
 RT "A gene pair from the human major histocompatibility complex encodes  
 large proline-rich proteins with multiple repeated motifs and a  
 single ubiquitin-like domain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378(1990).  
 [2]  
 SEQUENCE OF 1-1860 FROM N.A.  
 MEDLINE=93272029; PubMed=8499947;

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Cc Db 548 TPQVA-AAAPLTVS-----GGGGSSTSSSSGFASVPEPQLPSK 584
Cc Qy 122 DAEPPDLKVIITLSPGSDATAPAMPPEPDEGPTTPPEHSVPVPA TELGSLVTTKTAG- 180
Cc Db 585 EGGEPEPEV-----PPP-----TTPPVKVEPKKGIGPTROPPOGGLGY 624
Cc Qy 181 PEOQ 184
Cc Db 625 PKYQ 628
Cc
Cc RESULT 8
Cc HXB2 HUMAN
Cc ID HXB2 HUMAN STANDARD: PRT; 356 AA:
Cc AC P14652; P17485; P10913;
Cc DT 01-APR-1990 (Rel. 14, Created)
Cc DT 01-APR-1990 (Rel. 14, Last sequence update)
Cc DT 15-JUN-2002 (Rel. 41, Last annotation update)
Cc DE Homeobox protein Hox-B2 (Hox-2H) (Hox-2.8) (K8) .
Cc GN HOXB2 OR HOX2H.
Cc OS Homo sapiens (Human) .
Cc OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Cc OX NCBI_TaxID=9606;
Cc RN
Cc RP SEQUENCE FROM N.A.
Cc RX MEDLINE=90098876; PubMed=2574852;
Cc RA Acampora D., D'Esposito M., Faiella A., Pannese M.,
Cc RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.,
Cc RT "The human HOX gene family."
Cc RL Nucleic Acids Res. 17:10385-10402(1989) .
Cc RN [2]
Cc RP SEQUENCE OF 132-208 FROM N.A.
Cc RC TISSUE=Placenta;
Cc RX MEDLINE=89378558; PubMed=2570724;
Cc RA Ciampaglio A., Acampora D., Zappavigna V., Pannese M.,
Cc RA D'Esposito M., Care A., Faiella A., Stornaiuolo A., Russo G.,
Cc RA Simeone A., Boncinelli E., Peschle C.;
Cc RT "Differential expression of human HOX-2 genes along the anterior-
Cc RT posterior axis in embryonic central nervous system."
Cc RL Differentiation 40:191-197(1989) .
Cc RN [3]
Cc RP SEQUENCE OF 143-208 FROM N.A.
Cc RX MEDLINE=90215256; PubMed=2576652;
Cc RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
Cc RA Gaundino G., Stornaiuolo A., Caffero M., Faiella A., Simeone A.;
Cc RT "Organization of human class I homeobox genes."
Cc RL Genome 31:745-756(1989) .
Cc RN [4]
Cc RP SEQUENCE OF 143-202 FROM N.A.
Cc RX MEDLINE=88329001; PubMed=2901346;
Cc RA Kongswan K., Webb E., Housiaux P., Adams J.M.;
Cc RT "Expression of multiple homeobox genes within diverse mammalian
Cc RT haemopoietic lineages."
Cc RL EMBO J. 7:2131-2138(1988) .
Cc RN [5]
Cc RP SEQUENCE OF 1-42 FROM N.A.
Cc RX MEDLINE=95181447; PubMed=7876223;
Cc RA Vieille-Grosjean I., Huber P.;
Cc RT "Transcription factor GATA-1 regulates human HOXB2 gene expression in
Cc RT erythroid cells."
Cc RL J. Biol. Chem. 270:4544-4550(1995) .
Cc CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
Cc CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
Cc CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
Cc CC -1- SUBCELLULAR LOCATION: Nuclear.
Cc CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT
Cc CC 5-9 WEEKS FROM CONCEPTION.
Cc CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
Cc CC PROOSCIPEDIA SUBFAMILY.
Cc
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CC EMBL; X16665; CAA34655.1; -  
 DR EMBL; X16176; CAA34298.1; -  
 DR EMBL; X14571; CAA32709.1; -  
 DR EMBL; X78978; CAA55581.1; -  
 DR PIR; S07542; MTHU2H.  
 DR PIR; E37042; E37042.  
 DR HSSP; P14653; I872.  
 DR TRANSFAC; T03323; -  
 DR Genew; HGNC; 5113; HOXB2.  
 DR MIM; 142967; -  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR Prodom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS00071; HOMEBOX 2; 1.  
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT DOMAIN 94 99 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA\_BIND 143 202 HOMEBOX.  
 FT CONFLICT 136 138 PEA -> RRL (IN REF. 2).  
 SQ SEQUENCE 356 AA; 37913 MW; D7ACA0B3D5BEBF9 CRC64;

Query Match 11.0%; Score 106.5; DB 1; Length 356;  
 Best Local Similarity 24.7%; Pred. No. 0.99; Indels 89; Gaps 12;  
 Matches 56; Conservative 16; Mismatches 66; Indels 89; Gaps 12;

QY 5 PRS-LRGDAPA-----PTPCVPAECFDLVRHCVAAGLRTTRP-----KPA- 46  
 DB 66 PPSQKRAEGRALPPPPPPPLA-----APAPPEPPMKKKSAKPSQ 109  
 QY 47 GASSPAPRTALQPOSSVGAGAGALPLPG-----LL-----FG 80  
 DB 110 SATSSPASPASAVPAGVSGPADGLPEAGGGARLRRTAYNTQLLEKEFHFNYKYL 169  
 QY 81 APALGLALVLAIVLVGLVSW--RRQRRLRGASSSEADGDKDAPEDPKYI-----I 132  
 DB 170 RRRREIALLDLTERQVWFQNRMRMKRQTOHREPPDGPACGALEDICDPAEBPA 229  
 QY 133 LSPGSDATAPAM-----PP-----PG-----EDPGTTPG 158  
 DB 230 ASPGPGSASRAWEACHPPEVVPGLALSDPPRLAVRLGAGASBFG 276

RESULT 9  
 WASTL\_BOVIN STANDARD; PRT; 505 AA.  
 ID 095107;  
 AC 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Neural Wiskott-Aldrich syndrome protein (N-WASP).  
 GN WASL.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97050838; PubMed=8895577;  
 MIKI H., Mura K., Takenawa T.;

RT "N-WASP, a novel actin-depolymerizing protein, regulates the cortical  
 RT cytoskeletal rearrangement in a p12-dependent manner downstream of  
 RT tyrosine kinases";  
 RL EMBL J. 15:5326-5335(1996).

CC -1- FUNCTION: REGULATES ACTIN POLYMERIZATION BY STIMULATING THE ACTIN-  
 CC NUCLEATING ACTIVITY OF THE ACTIN-RELATED PROTEIN 2/3 (ARP2/3)  
 CC COMPLEX.  
 CC -1- SUBUNIT: BINDS ACTIN AND ARP2/3 COMPLEX; INTERACTS WITH CDC42  
 CC BINDS TO SH3 DOMAINS OF ASH/GRB2.  
 CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 WH1 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 WH2 DOMAINS.  
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CC EMBL; D67066; BA011082.1; -  
 DR InterPro; IPR000095; PARDOX/RhoGTPase.  
 DR InterPro; IPR000697; RanBP1\_WASP.  
 DR InterPro; IPR001960; WH1.  
 DR InterPro; IPR003124; WH2.  
 DR Pfam; PF00568; WH1; 1.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF02205; WH2; 2.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00461; WH1; 1.  
 DR SMART; SM00246; WH2; 2.  
 DR PROSITE; PS50108; CRIB; 1.  
 KW Actin-binding; Repeat.  
 FT DOMAIN 34 138 WH1.  
 FT DOMAIN 203 216 CRIB.  
 FT DOMAIN 277 392 PRO-RICH.  
 FT DOMAIN 405 422 WH2 1.  
 FT DOMAIN 433 450 WH2 2.  
 FT DOMAIN 486 505 ASP-RICH.  
 SQ SEQUENCE 505 AA; 54671 MW; 54B83B48F1CB3B8 CRC64;

Query Match 10.7%; Score 103; DB 1; Length 505;  
 Best Local Similarity 23.6%; Pred. No. 2.3; Indels 84; Gaps 7;  
 Matches 41; Conservative 4; Mismatches 45; Indels 84; Gaps 7;

QY 5 PSLRGDAPAPTPC--VPAECFDLVRHCVAAGLRTTRPKPA-----GASSPAPRTALQ 59  
 DB 301 PEPARGGAPPPPPSRAPTA-----PPPPPSRGVAGAPPPPPRMP 345  
 QY 60 QESVAGAGAGALPLGLFGAPALGLALVLAIVLVGWSRRQRRLRGASSSEADG 119  
 DB 346 -----PLPAL-----PSSAPSG 357  
 QY 120 DKDAPEPLDKVILISPGISDATAPAMPPGEGDPTTP-----GHSVPVPA 165  
 DB 358 PPPPPPL-----SVSGSVAPPPPPPPPPPPPPGPGGLPSGDQVPTPA 403

RESULT 10  
 ICP0\_HSVBK STANDARD; PRT; 676 AA.  
 ID P29836;  
 AC 01-APR-1993 (Rel. 25; Created)  
 DT 01-APR-1993 (Rel. 25; Last sequence update)  
 DT 16-OCT-2001 (Rel. 40; Last annotation update)  
 DE Trans-acting transcriptional protein ICP0 (p135 protein) (IER  
 DE 2.9/IER.6).  
 GN ICP0.  
 OS Bovine herpesvirus type 1 (strain K22).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicelloviruses.  
 OC NCBI\_TaxID=31519;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92219360; PubMed=1313901;
RA Wirth U.V., Friefel C., Vogt B., Vojtek C., Paces V., Schwyzler M.
RT "Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1
RT are 3' coterminal and encode a putative zinc finger transcription
RT protein."
RL J. Virol. 66:2763-2772(1992).
CC -1- PTM: THE STRONGLY ACIDIC REGION MIGHT SERVE AS A TRANSCRIPTIONAL
CC ACTIVATION DOMAIN, POSSIBLY REGULATED THROUGH PHOSPHORYLATION BY
CC CASEIN KINASE II.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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EMBL, M84464; AAA46061.1; -.
DR F1R; A38209; EDBE22.
DR HSSP; P28990; 1CHC.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
DR DNA-binding; Early protein; Repressor; Phosphorylation.
DR ZN FING 13 52 RING-TYPE.
FT DOMAIN 284 331 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 676 AA; 67701 MW; 98B0683C9BFC65D CRC64;

Query Match 10.6%; Score 102.5; DB 1; Length 676;
Best Local Similarity 29.4%; Pred. No. 3.3;
Matches 60; Conservative 14; Mismatches 79; Indels 51; Gaps 11;

QY 7 SURGRAPAPTPVPECEPDLVHRCVACG-----LIRTRPRXP 45
DB 353 STRGRQTPVQPPRPS-----LARR--PCGRAAVAPSPSSRSGRRDRPLPAAPRAAP 405
QY 46 AG---ASSPAPRPAALPOESVGAGAGAAALPLPGLLFGAPALLGLALVLVLVVG---LV 99
DB 406 AAOARACSPPEPR-----EEGRAGLGVAAAGETGCMGVGSEEGGERAKILSGAGPPRVQ 460
QY 100 SWRRQRRL-RGASSAEPDGDGDAPEDPLDKVILSPGISDATA-PAMPPGEGDPTTPP 157
DB 461 ARRRRTTELDRAPTPAPAP---APAPAPISTMIDLTR--ANAPARAPADPAPAAALGPALA 514
QY 158 GHSVPVPATLSTELVTTKTAP 181
DB 515 GAQIGTPA-----AAAAVTAAAAAP 534

RESULT 11
AREA_PENCH STANDARD; PRT; 725 AA.
ID AREA_PENCH
AC Q01582;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nitrogen regulatory protein area (Nitrogen regulator nre).
GN AREA OR NRE.
OS Penicillium chrysogenum.
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_Taxid=5076;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95308537; PubMed=7788718;

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RA Haas H., Bauer B., Redl B., Stoeffler G., Marzluft G.A.;
RT "Molecular cloning and analysis of nre, the major nitrogen regulatory
RT gene of Penicillium chrysogenum."
RL Curr. Genet. 27:150-158(1995)
CC -1- FUNCTION: MAJOR NITROGEN REGULATORY PROTEIN.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.
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CC or send an email to license@isb-sib.ch).
EMBL, U02612; AA83400.1; -.
DR HSSP; P17429; 4GAT.
DR InterPro; IPR000679; Znf_GATA.
DR Pfam; PF00320; GATA; 1.
DR PRINTS; PR00619; GATAZNFINGER.
DR SMART; SM00401; ZNF_GATA; 1.
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
DR PROSITE; PS50114; GATA_ZN_FINGER_2; 1.
DR Transcription regulation; Activator; DNA-binding; Zinc-finger;
DR Nuclear protein; Nitrate assimilation.
FT ZN FING 525 549 GATA-TYPE.
SQ SEQUENCE 725 AA; 76848 MW; 45C24148F1FAD43 CRC64;

Query Match 10.6%; Score 102.5; DB 1; Length 725;
Best Local Similarity 27.0%; Pred. No. 3.5;
Matches 47; Conservative 13; Mismatches 59; Indels 55; Gaps 7;

QY 32 CVACGL-----LIRTRPRKAGASP-----APRATL 57
DB 546 CNACGLFLKGVNPPLSLKTDVYIKRNRSSANLITVGTSSSKSKSRKNSIQHPSTSI 605
QY 58 QPQ-----ESVGAGAGAAALPLPGL--LFGAPALLGLALVLVLVGLVSWRRQRRLGA 111
DB 606 SSRNMTSESPSPINSSTLKGQGVPIAAPPKSPGAGVAGARQGVAPARRQRLLEA 665
QY 112 SGAEPDGDGD---APEPLDKVILSPGISDATA-PAMPPGEGDPTTPPGHSV 161
DB 666 PAGSEPDADDSPEKSAAPPSRSKVPL-----APAMAPPA---AANPANHSI 708

RESULT 12
YQ35_CAEEL STANDARD; PRT; 317 AA.
ID YQ35_CAEEL
AC Q09456;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative cuticle collagen C0965.5.
GN C0965.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Br1etol N2;
RA Palmer S.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
CC PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
CC BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).
CC -1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CC CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
CC LINKS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CUTICULAR COLLAGEN FAMILY.
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DR EMBL; 246791; CAA86758.1; -  
 DR WormPep; C09G5.5; CE01485.  
 DR InterPro; IPR002486; Col cuticle\_N.  
 DR InterPro; IPR000087; Collagen.  
 DR Pfam; PF01891; Collagen; 3.  
 DR Pfam; PF01884; Col cuticle\_N; 1.  
 DR Hypothetical protein; Cuticle; Connective tissue; Repeat;  
 KW Multigene family; Collagen.  
 FT DOMAIN 92 124 TRIPLE-HELICAL REGION.  
 FT DOMAIN 137 199 TRIPLE-HELICAL REGION.  
 FT DOMAIN 202 264 TRIPLE-HELICAL REGION.  
 FT SEQUENCE 317 AA; 31283 MW; 685DCF24612707BB CRC64;

Query Match 10.6%; Score 102; DB 1; Length 317;  
 Best Local Similarity 26.7%; Pred. No. 1.8;  
 Matches 54; Conservative 10; Mismatches 68; Indels 70; Gaps 12;

QY 4 GRSLSRGDAPAPPTPCVP--AECFDLIVRHCVACGLLRTPR--PKPAGA-SSPAPR-----54  
 DB 101 GDRGLDGGCPGAPGKPGQPGVAGPAHHQOQECIKC-----PQAGAPGAPGAPGPGGPGNG 155  
 QY 55 TLQGPQESVAG-----AGEAALP---LPGILFGAPALLGLALVIALVGLVSWRR 103  
 DB 156 NGAAPAHGGGGGPPGPPGAPGAGSGAGAPGPNP-GRPGQG-----Q 198  
 QY 104 RQRRLRGASSAAPDDKDAPEPLDKVILISPGISDATAPAMP-----PGEPP 152  
 DB 199 RRRGLPFGSGRPGCPGPPAPG-----QPGSSGTPGAPGPPGPPGPGGPGHFGDQG 250  
 QY 153 GTTPPGHS-----VEVPA 165  
 DB 251 QGAPGNDGAPGSDAAYCPCPA 272

RESULT 13  
 DBP\_MOUSE STANDARD; PRT; 325 AA.  
 ID DBP\_MOUSE 060925;  
 AC 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 GN D-site-binding protein (Albumin D box-binding protein).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv; TISSUE=Liver;  
 RL Lee Y.H., Oguchi H., Gonzalez F.J.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: THIS TRANSCRIPTIONAL ACTIVATOR RECOGNIZES AND BINDS TO  
 CC THE SEQUENCE 5'-RTTAGTAA-3' FOUND IN THE PROMOTER OF GENES SUCH  
 CC AS ALBUMIN, CYP2A4 AND CYP2A5. IT IS NOT ESSENTIAL FOR CIRCADIAN  
 CC RHYTHM GENERATION, BUT MODULATES IMPORTANT CLOCK OUTPUT GENES. MAY  
 CC BE A DIRECT TARGET FOR REGULATION BY THE CIRCADIAN PACEMAKER  
 CC COMPONENT CLOCK. MAY AFFECT CIRCADIAN PERIOD AND SLEEP REGULATION  
 CC (BY SIMILARITY).  
 CC -1- SUBUNIT: BINDS DNA AS A HOMODIMER OR A HETERODIMER. CAN FORM A  
 CC HETERODIMER WITH TEF (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE SUPRACHIASMATIC NUCLEI (SCN)  
 CC AND IN MOST PERIPHERAL TISSUES, WITH A STRONG CIRCADIAN  
 CC RHYTHMICITY.  
 CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY. PAR SUBFAMILY.

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DR EMBL; U29762; AAA73924.1;  
 DR MGD; MGI:94866; DBP.  
 DR InterPro; IPR004827; TP\_bZIP.  
 DR SMART; SM00338; BRLZ; 1.  
 DR DNA-binding; Transcription regulation; Activator; Nuclear protein;  
 KW Biological rhythms.  
 FT DOMAIN 129 135 POLY-PRO.  
 FT DOMAIN 156 161 POLY-SER.  
 FT DOMAIN 188 239 PRO-RICH (PROLINE/ACIDIC REGION (PAR)).  
 FT DNA BIND 258 277 BASIC MOTIF.  
 FT DOMAIN 290 304 LEUCINE-ZIPPER.  
 FT SEQUENCE 325 AA; 34428 MW; 58F7067DD1238B06 CRC64;

Query Match 10.6%; Score 102; DB 1; Length 325;  
 Best Local Similarity 26.1%; Pred. No. 1.8;  
 Matches 54; Conservative 14; Mismatches 77; Indels 62; Gaps 9;

QY 4 GRSLSRGDAPAPPTPCVP-----ECFDL---IVRHCVACGLLRTPRKPAG 47  
 DB 83 GGGSPRSGSGVAGSLPAPLIMERTPPGQVEYVDLAFLEH---GL--PPPPPPG 136  
 QY 48 ASSPAPRTALQPOSVAGAGEAALP--LPGILFGAPALLGLALVIALVGLVSWRRQ 105  
 DB 137 GLSPAPSPAPRTAPBPGGSCSSSPRSSPG---HAP-----R 172  
 QY 106 RRLRGASSAAPDDKDAPEPLDKVILISPGISDATAPAMP-----PGEPP 152  
 DB 173 ATLGAAGHRAGLTSRDTPSPVD-----PDVEVILMTFEPDADLALSIPGHETFDPR 226  
 QY 166 TELGSTELY-----TTKTAGPEEQ 184  
 DB 227 RHRFSEELKQPIKKAKKQVQVPEEQ 253

RESULT 14  
 DBP\_RAT STANDARD; PRT; 325 AA.  
 ID DBP\_RAT P16443;  
 AC 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 GN D-site-binding protein (Albumin D box-binding protein) (D site albumin  
 DE promoter binding protein 1).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCB1\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Liver;  
 RX MEDLINE=90235277; PubMed=2331750;  
 RA Mueller C.R., Maitre P., Schibler U.;  
 RT "DBP, a liver-enriched transcriptional activator, is expressed late  
 RT in ontogeny and its tissue specificity is determined  
 RT posttranscriptionally.";  
 RT Cell 61:279-291 (1990).  
 RN [2]  
 RP REVISIONS.  
 RA Mueller C.R., Maitre P., Schibler U.;  
 RL Cell 65:915-915 (1991).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=9439627; PubMed=10508692;



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Qy 10 GRDAPAPTECVPAECFDLIV---RHCVACGLIRTPRPKAGASSPAPRTALQPCEVGA 65
Db 165 GLQAFGFLPAPAGDEBDLLQAVQSCCLADHLLTA-----SWGADVPITKA-----P 211
Qy 66 GAGEAALPPLGILLFGAPALGLALVLAIVLVGVSVRRRORRLRGASSAEPDGDKAPE 125
Db 212 GEGQEGPLPLTGACAGGP-----GLPAGELYGWAVEITPSPGPQAPALTTGEAAPE 262
Qy 126 -PLDKVITLSPGISDATAPAMPPPG 149
Db 263 SPHQAEPLYLSPSPSACTAVQEBSPG 287

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